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Scientific and Technical Information Center

## SEARCH REQUEST FORM

(STIC)

Requester's Full Name: JANE ZARA Examiner #: 77518 Date: 7/11/05  
 Art Unit: 1635 Phone Number: 2-0765 Serial Number: 091735363  
 Location (Bldg/Room#): 2D28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK Me  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Perceptually useful synthetic design  
 Inventors (please provide full names): Phillips et al.

Earliest Priority Date: 12/12/00

## Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seg ID Nos

8, 10, 25, 42, 43 + 45

For Seg 8, please limit to size of 3 NTS.

For Seg 10, please limit to size of 6 NTS.

For Seg 42, please limit to size of 6 NTS

For Seg 43, please limit size to 6 NTS.

For Seg 45, please limit size to 6 NTS.

Please search references + regular date lines. Thanks.

STAFF USE ONLY		Type of Search	Vendors and cost where applicable	
Searcher:		NA Sequence (#)	STN	Dialog
Searcher Phone #:		AA Sequence (#)	Questel/Orbit	Lexis/Nexis
Searcher Location:		Structure (#)	Westlaw	WWW/Internet
Date Searcher Picked Up:		Bibliographic	In-house sequence systems	
Date Completed:		Litigation	Commercial	Oligomer
Searcher Prep & Review Time:		Fulltext	Interference	SPDI
Online Time:		Other	Score/Length Other (specify)	

Thu Jul 21 10:31:17 2005

us-09-735-363a-25.szlm6.rnpn

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds  
(without alignments)  
23.814 Million cell updates/sec

Title: US-09-735-363a-25  
Perfect score: 6  
Sequence: 1 gggtgg 6  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 16353451 seqs, 2487343176 residues  
Total number of hits satisfying chosen parameters: 2336  
Minimum DB seq length: 0  
Maximum DB seq length: 6  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries  
Database : Pending Parents NA New:  
1: /cgn2\_6/ptodata/1/pna/pct\_new\_comb.seq.\*  
2: /cgn2\_6/ptodata/1/pna/pct\_new\_comb.seq2.\*  
3: /cgn2\_6/ptodata/1/pna/us06\_new\_comb.seq.\*  
4: /cgn2\_6/ptodata/1/pna/us07\_new\_comb.seq.\*  
5: /cgn2\_6/ptodata/1/pna/us08\_new\_comb.seq.\*  
6: /cgn2\_6/ptodata/1/pna/us09\_new\_comb.seq.\*  
7: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq.\*  
8: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq2.\*  
9: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq3.\*  
10: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq4.\*  
11: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq5.\*  
12: /cgn2\_6/ptodata/1/pna/us10\_new\_comb.seq6.\*  
13: /cgn2\_6/ptodata/1/pna/us11\_new\_comb.seq.\*  
14: /cgn2\_6/ptodata/1/pna/us11\_new\_comb.seq2.\*  
15: /cgn2\_6/ptodata/1/pna/us11\_new\_comb.seq3.\*  
16: /cgn2\_6/ptodata/1/pna/us11\_new\_comb.seq4.\*  
17: /cgn2\_6/ptodata/1/pna/us60\_new\_comb.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match length	DB ID
.....	.....	.....	.....

Thu Jul 21 10:31:18 2005

us-09-735-363a-42.szlm6.rnpm

Gendcore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds  
(without alignments)  
136.380 Million cell updates/sec

Title: US-09-735-363A-42  
Perfect score: 6  
Sequence: 1 ggaagg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 100 summaries

Database : Pending\_Patents\_NA\_Main:\*

GenCore version 5.1.6  
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## OM\_nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds

(without alignments)

23.814 Million cell updates/sec

Title: US-09-735-363A-42  
Perfect score: 6  
Sequence: 1 ggaagg 6

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16351451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 100 summaries

Database : Pending Patents NA\_New:  
 1: /cgmn2\_6/picodata/1/pna/PCT NEW COMB.seq:/\*  
 2: /cgmn2\_6/picodata/1/pna/PCT NEW COMB.seq2:/\*  
 3: /cgmn2\_6/picodata/1/pna/US16\_NEV COMB.seq:/\*  
 4: /cgmn2\_6/picodata/1/pna/US07 NEW COMB.seq:/\*  
 5: /cgmn2\_6/picodata/1/pna/US08 NEW COMB.seq:/\*  
 6: /cgmn2\_6/picodata/1/pna/US09 NEW COMB.seq:/\*  
 7: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 8: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 9: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 10: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 11: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 12: /cgmn2\_6/picodata/1/pna/US10 NEW COMB.seq:/\*  
 13: /cgmn2\_6/picodata/1/pna/US11 NEW COMB.seq:/\*  
 14: /cgmn2\_6/picodata/1/pna/US11 NEW COMB.seq2:/\*  
 15: /cgmn2\_6/picodata/1/pna/US11 NEW COMB.seq3:/\*  
 16: /cgmn2\_6/picodata/1/pna/US11 NEW COMB.seq4:/\*  
 17: /cgmn2\_6/picodata/1/pna/US60 NEW COMB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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/ Thu Jul 21 10:31:20 2005

us-09-735-363a-43.sz1m6.rnpn

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds

(without alignments)  
136.380 Million cell updates/sec

Title: US-09-735-363A-43  
Perfect score: 6  
Sequence: 1 99CC99 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : Pending\_Patents\_NA\_Main:\*

Thu Jul 21 10:31:22 2005

us-09-735-363a-45.sz1m6.rnpn

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds  
(without alignment(s))  
136.380 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6  
Sequence: 1 999agg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554813 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:

13936

Minimum DB seq length: 0

Maximum DB seq.length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents NA Main:\*

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## OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds

(without alignments)

23.814 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 ggccgg 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16353451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

```

Pending Patents NA New:*
1: /cgn2_6/ptodata/71/pna/pct_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/us06_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/us07_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/us08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq3:*
10: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq4:*
11: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq5:*
12: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq6:*
13: /cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq2:*
15: /cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq3:*
16: /cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq4:*
17: /cgn2_6/ptodata/1/pna/us60_NEW_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
...				

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds  
 (without alignments)  
 23.814 Million cell updates/sec

Title: US-09-735-363A-45  
 Perfect score: 6  
 Sequence: 1 999999 6.  
 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0  
 Searched: 16353451 seqs, 2487343176 residues  
 Total number of hits satisfying chosen parameters: 2336  
 Minimum DB seq length: 0  
 Maximum DB seq length: 6  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

<b>Database :</b>	Pending Patents_NA_New:*
1:	/cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq:*
2:	/cgn2_6/ptodata/1/pna/pct_NEW_COMB.seq2:*
3:	/cgn2_6/ptodata/1/pna/us07_NEW_COMB.seq:*
4:	/cgn2_6/ptodata/1/pna/us07_NEW_COMB.seq:*
5:	/cgn2_6/ptodata/1/pna/us08_NEW_COMB.seq:*
6:	/cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:*
7:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq:*
8:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq2:*
9:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq2:*
10:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq3:*
11:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq4:*
12:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq5:*
13:	/cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq6:*
14:	/cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq:*
15:	/cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq3:*
16:	/cgn2_6/ptodata/1/pna/us11_NEW_COMB.seq4:*
17:	/cgn2_6/ptodata/1/pna/us60_NEW_COMB.seq:*

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Thu Jul 21 10:31:15 2005

us-09-735-363a-10.sz1m6.rnpm

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds

(without alignment)

136.380 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 gtgggt 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554973 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending\_Patents\_NA\_Main:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds

(without alignments)  
23.814 Million cell updates/sec

Title: US-09-735-363A-10  
Perfect score: 6  
Sequence: 1 gtgtgt 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16353451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Minimum DB seq length: 0  
Maximum DB seq length: 6

Listing first 100 summaries

Database : Pending Parents NA New:  
 1: /cgn2\_6/ptodata/1/pna/PT1\_NEW\_COMB.seq:/\*  
 2: /cgn2\_6/ptodata/1/pna/PT2\_NEW\_COMB.seq:/\*  
 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:/\*  
 4: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:/\*  
 5: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:/\*  
 6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:/\*  
 7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:/\*  
 8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq2:/\*  
 9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq3:/\*  
 10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq4:/\*  
 11: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq5:/\*  
 12: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq6:/\*  
 13: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq:/\*  
 14: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq2:/\*  
 15: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq3:/\*  
 16: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq4:/\*  
 17: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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Run on: July 20, 2005 20:42:19 ; Search time 2266 Seconds  
 DOM nucleic - nucleic search, using sw model  
 (without alignment) rpsblastn

Title: US-09-735-363A-8  
 Perfect score: 3  
 Sequence: 1 9tg 3  
 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0  
 Searched: 45554873 seqs, 20411521753 residues  
 Total number of hits satisfying chosen parameters: 2500  
 Minimum DB seq length: 0  
 Maximum DB seq length: 3  
 Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 100 summaries  
 Pending Patents\_NA\_Main: \*  
 Database: 1 /~/\_Patents\_NA\_Main: \*

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OM nucleic - nucleic search, using sw model.

Run on: July 20, 2005, 20:46:47 ; Search time 644 Seconds  
(without alignments)

23,168 Million cell updates/sec

Title: US-09-735-363A-8  
Perfect score: 3  
Sequence: 1 gtg 3

Scoring table: IDENTITY\_NUC  
Gapop 1.0 , Gapext 1.0

Searched: 16351682 seqs, 2486654067 residues

Total number of hits satisfying chosen parameters: 132

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents NA New /\*  
1: /cgn2\_6/ptodata/72/pna/pct\_NEW\_COMB.seq:/\*  
2: /cgn2\_6/ptodata/2/pna/pct\_NEW\_COMB.seq2:/\*  
3: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:/\*  
4: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:/\*  
5: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:/\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:/\*  
7: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:/\*  
8: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:/\*  
9: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq3:/\*  
10: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq4:/\*  
11: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq5:/\*  
12: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq6:/\*  
13: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq:/\*  
14: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq2:/\*  
15: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq3:/\*  
16: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq4:/\*  
17: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match Length	DB ID	Description
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Thu Jul 21 10:31:17 2005

US-09-735-363a-25.sz1m6.rnpn

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds

(without alignments)

136.380 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 99999 6

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending\_Patents\_NA\_Main:\*